



841 SFARTVNKEYPGLADPVFRTLVSQILDQAEPLLSSLSSEVVTVFOYYSYFTSHGVSDLE 900
901 SYLSQLARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLALLLTREDNEVSEA 960
961 VTLYLAAASKNQHFREKALLYCEALTTKTNLQLQKAACIALKILEATESIKMLVTLCOQSD 1020
1021 TEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF 1068

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO:37)

Bottom sequence: predicted Diff40 short form NCBI (NP_056948) (SEQ ID NO:38)

FIG. 6C

REPLACEMENT SHEET

[illegible]

Top sequence: predicted Diff40 Short form (RefSeq NP_056948) (SEQ ID NO: 40)
Bottom sequence: T2DM-1b (SEQ ID NO: 4)

FIG. 8B

841 SFARTVNKEYPGLADPVFRTLVSQILDQAEPLLSLSSSEVTVFQYYSYFTSHGVSDLE 900
 901 SYLSQLARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRTLALLLTREDNEVSEA 960
 961 VTLYLAASKNQHFREKALLYCEALTKTNLQLOKAAACLALKILEATESIKMLVTLQCSD 1020
 1021 TEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF 1068

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO: ~~f23~~+37)
 Bottom sequence: predicted Diff40 short form NCBI (NP_056948) (SEQ ID
 NO: ~~f24~~+38)

FIG. 6C

710 RGHLSALETDTGVGTSVAGSPLPLTTGNESLDITIVRHLQYCTQLVQQIVFSSKTPFVA 769
 602SSLKASSRELTAGAPELDVLLMVHLQVCKALLQKLASPNLSRLVQ 646
 770 RSLLEKLSRQIQVMEKLAASVDENIGNISSVVEAIPFHKKLSLSFWTKCCSPVGVYHS 829
 647 ECLLEEVAQQKHVLETLSVLDFEKVGKATSIIEEIPQASRTKGCLKLWRGCTGPGRVLS 706
 7
 830 PADRVMKQLEASFARTVNKEYPGLADPVFRTLVSQILDQAEPLSSSSLSSE.VVTVFQYY 888
 707 PATLLNQKKTFQHRVRGKYPGQLEIACRRLLQVSCGGLPGAGLPQEEQIITWFOFH 766
 889 SYFTSHGVSDLESYLSQARQVSMVQTLQSLRDEKLLQTMSDLAPSNLLAQQEVLRAL 948
 767 SYLQQRQSVSDLEKHFQTLTKEVTLIEELHCAGQAKVVRKLGQKRLGQLPQTLRAWAL 826
 949 LLTREDNEVSEAVTLYLAAASKNQHFREKALLYCEALTKTNLQKAAACIALKILEATE 1008
 827 LQLDGTPRCRAASARLAGAVRNRSFREKALLFYTNALAENDARLQQAACIALKHLKGIE 886
 1009 SIKMLVTLCQSDTEEIRNVASETLLSLGEDGRLAYEQLDK 1048
 887 SIDQTASLCQSDLEAVRAARETTLSFGEKGRLAFAEKMDKLCSEQREVFCEADVEITIF 946

Top sequence: predicted Diff40 long form (BAA20840) (SEQ ID NO: ~~123~~39)
 Bottom sequence: T2DM-1a (SEQ ID NO:2)

FIG. 7C

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358 FFSNLPDDIFENGKAAEEKMPLSLFSDLPNGDCALTSHTGSPSNSTNPEITITPAEF. 416
      : | |           . | . | | | | . | | . | | : |
357 YLSVL.....QQPTQOAL..LLGGPRATSILSYLSDSDLRGP SLRSQS QELP 401
      . . . . .
417 NLSSLASONEGMDDTSSASSRNSLG...EQEPPKSHLKEEDPEEPKPAPASEACRRQS 473
      : | : | :: | | .. | | . : | | | | | | | |
402 EMDSFSEDPRDTETSTSASTSDVGFLPLTFGPHASIEEEEAREDP LPPGLLEMA..HLS 459
      . . . . .
474 SGAGAE 479
      | | |
460 GGPFAEQPGWRNLGGESP LPQGSLFHSGTASSSQNGHEEGATGDREDGPGVALEG PLQE 519
      . . . . .
520 VLELLRP TDSTQPQLRELEYQV LGFRDRLKVWPP RPGRWP C FADGMTGT SRGLWGHA AWA 579
      . . . . .
580 DILASPLRD LGGPC LSGPWFP PH LASCDNN SPHG AQ EDF KSSQ 621

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Top sequence: predicted Diff40 Short form (RefSeq NP_056948) (SEQ ID NO: [24]
40)
Bottom sequence: T2DM-1b (SEQ ID NO: 4)